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DATE: 04/26/2001

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,209A

Input Set : A:\190337.txt
Output Set: N:\CRF3\04262001\I530209A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Inze, Dirk

6 De Veylder Lieven
7 De Almeida Janice

9 (iii) TITLE OF INVENTION: A novel mitogenic cyclin and uses thereof

11 (iii) NUMBER OF SEQUENCES: 4

C--> 13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Nixon Peabody LLP

15 (B) STREET: 990 Stewart Avenue

16 (C) CITY: Garden City

17 (D) STATE: New York, New York

C--> 18 (F) ZIP: 11530

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/530,209A

C--> 28 (B) FILING DATE: 13-Jun-2000

29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: EP PCT/EP98/06749

33 (B) FILING DATE: 23-OCT-1998

34 (A) APPLICATION NUMBER: EP 97.203.303.9

35 (B) FILING DATE: 24-OCT-1997

38 (2) INFORMATION FOR SEQ ID NO: 1:

40 (i) SEQUENCE CHARACTERISTICS:

41 (A) LENGTH: 927 base pairs

42 (B) TYPE: nucleic acid

43 (C) STRANDEDNESS: double

44 (D) TOPOLOGY: linear

46 (ii) MOLECULE TYPE: cDNA

48 (iii) HYPOTHETICAL: NO

50 (ix) FEATURE:

51 (A) NAME/KEY: CDS

52 (B) LOCATION: 1..927

54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

56 ATG GCA GAG GAA AAT CTA GAA CTG AGT CTT TTA TGT ACA GAG AGC AAC	48
57 Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn	
58 1 5 10 15	
60 GTT GAT GAT GAG GGC ATG ATT GTT GAC GAA ACT CCG ATT GAA ATT TCG	
61 Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser	
62 20 25 30	
64 ATT CCT CAG ATG GGT TTT TCT CAA TCG GAG AGT GAG GAG ATT ATC ATG	
65 Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Glu Ile Ile Met	

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66	35	40	45	
68	GAG ATG GTG GAG AAG GAG AAG CAG CAT TTG CCA AGT GAT GAT TAC ATC			192
69	Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile			
70	50	55	60	
72	AAG AGA CTT AGA AGT GGA GAT TTG GAT TTG AAT GTT GGA AGA AGA GAT			240
73	Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp			
74	65	70	75	80
76	GCC CTC AAT TGG ATT TGG AAG GCT TGT GAA GTA CAC CAG TTT GGA CCA			288
77	Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro			
78	85	90	95	
80	TTG TGT TTT TGC TTA GCA ATG AAC TAC TTG GAT CGA TTC TTA TCG GTT			336
81	Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val			
82	100	105	110	
84	CAT GAT TTG CCT AGT GGC AAA GGT TGG ATA TTG CAG TTG TTG GCT GTG			384
85	His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val			
86	115	120	125	
88	GCT TGT TTA TCA TTG GCA GCC AAA ATT GAA GAA ACT GAA GTT CCA ATG			432
89	Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met			
90	130	135	140	
92	TTG ATA GAT CTT CAG GTT GGA GAT CCT CAG TTT GTG TTT GAG GCT AAA			480
93	Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys			
94	145	150	155	160
96	TCA GTC CAA AGA ATG GAG CTT TTG GTG TTG AAC AAA TTG AAA TGG AGA			528
97	Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg			
98	165	170	175	
100	TTG AGA GCA ATA ACT CCA TGC TCA TAC ATA AGA TAT TTC CTG AGA AAG			576
101	Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys			
102	180	185	190	
104	ATG AGT AAA TGT GAT CAA GAA CCA TCC AAC ACA TTG ATA TCT AGA TCA			624
105	Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser			
106	195	200	205	
108	TTA CAA GTG ATA GCC AGC ACA ACC AAA GGT ATT GAC TTT TTG GAG TTT			672
109	Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe			
110	210	215	220	
112	AGA CCT TCT GAA GCT GCT GCT GTG GCA CTT TCT GTT TCT GGA GAA			720
113	Arg Pro Ser Glu Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu			
114	225	230	235	240
116	TTG CAG AGA GTA CAC TTT GAC AAC TCT TCC TTC TCT CCT CTT TTC TCA			768
117	Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser			
118	245	250	255	
120	CTA CTT CAA AAG GAG AGA GTG AAG AAG ATA GGG GAA ATG ATA GAG AGT			816
121	Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser			
122	260	265	270	
124	GAT GGC TCA GAC TTA TGT TCA CAA ACA CCC AAT GGG GTT TTA GAA GTA			864
125	Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val			
126	275	280	285	
128	TCG GCT TGT TGT TTC AGC TTT AAG ACC CAT GAT TCT TCT TCT TCT TAT			912
129	Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr			
130	290	295	300	

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132	ACA CAT CTT TCT TAA	927
133	Thr His Leu Ser	
134	305	
137	(2) INFORMATION FOR SEQ ID NO: 2:	
139	(i) SEQUENCE CHARACTERISTICS:	
140	(A) LENGTH: 308 amino acids	
141	(B) TYPE: amino acid	
142	(D) TOPOLOGY: linear	
144	(ii) MOLECULE TYPE: protein	
145	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
147	Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn	
148	1 5 10 15	
150	Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser	
151	20 25 30	
153	Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met	
154	35 40 45	
156	Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile	
157	50 55 60	
159	Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp	
160	65 70 75 80	
162	Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro	
163	85 90 95	
165	Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val	
166	100 105 110	
168	His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val	
169	115 120 125	
171	Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met	
172	130 135 140	
174	Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys	
175	145 150 155 160	
177	Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg	
178	165 170 175	
180	Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys	
181	180 185 190	
183	Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser	
184	195 200 205	
186	Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe	
187	210 215 220	
189	Arg Pro Ser Glu Ala Ala Val Ala Leu Ser Val Ser Gly Glu	
190	225 230 235 240	
192	Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser	
193	245 250 255	
195	Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser	
196	260 265 270	
198	Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val	
199	275 280 285	
201	Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr	
202	290 295 300	
204	Thr His Leu Ser	

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205 305
208 (2) INFORMATION FOR SEQ ID NO: 3:
210 (i) SEQUENCE CHARACTERISTICS:
211 (A) LENGTH: 25 base pairs
212 (B) TYPE: nucleic acid
213 (C) STRANDEDNESS: single
214 (D) TOPOLOGY: linear
216 (ii) MOLECULE TYPE: other nucleic acid
217 (A) DESCRIPTION: /desc = "oligonucleotide"
219 (iii) HYPOTHETICAL: YES
221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
223 GAACACTCGA GTGTAATGGC AGAGG 25
227 (2) INFORMATION FOR SEQ ID NO: 4:
229 (i) SEQUENCE CHARACTERISTICS:
230 (A) LENGTH: 26 base pairs
231 (B) TYPE: nucleic acid
232 (C) STRANDEDNESS: single
233 (D) TOPOLOGY: linear
235 (ii) MOLECULE TYPE: other nucleic acid
236 (A) DESCRIPTION: /desc = "oligonucleotide"
238 (iii) HYPOTHETICAL: YES
240 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
242 CATCATACTA GTTATAATAA TGTAAG 26

VERIFICATION SUMMARY

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Input Set : A:\190337.txt

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L:13 M:220 C: Keyword misspelled or invalid format, [(iv) CORRESPONDENCE ADDRESS:]
L:18 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]